

12/95

## SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: David Fox Examiner #: 65401 Date: 5/12/04  
 Art Unit: 1638 Phone Number: 20795 Serial Number: 09791-023  
 Mail Box and Bldg/Room Location: REM 209 Results Format Preferred (circle): PAPER DISK E-MAIL  
2018

If more than one search is submitted, please prioritize searches in order of need. MEJ

\*\*\*\*\*  
 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

NO HITS

Earliest Priority Filing Date: 3/99

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

please search  
 renewed OF SEQ ID NO: 2  
 stay  
 Thank you

2NA-271

MEJ 5/13  
14

## STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>Arnold</u>	NA Sequence (#) <u>1</u>	STN _____
Searcher Phone #: <u>20530</u>	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>5/12/04</u>	Bibliographic _____	De Link _____
Date Completed: <u>5/17/04</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Copyright (C) 1993 - 2004 Compugen Ltd.

GenCore version 5.1.6

GenCore version 5.1.6

icletic - nucleic search, using sw model

in: May 16, 2004, 10:21:20; Search time 2469 Seconds  
(without alignments)  
3956.201 Million cell updates/sec

ct score: 271.4

nce: 1 gtagatgatctcttaacaa.....ctactctagctctctctta 271

ng table: IDENTITY NUC

Gspop 10.0, Gapext 1.0

hed: 3470272 segs, 2167151695 residues

number of hits satisfying chosen parameters: 6940544

um Dli seq length: 0

um DB seq length: 2000000000

processing: Minimum Match 0.0

Listing first 45 summaries

ase :

1: gb-hu.\*

2: gb-hu.\*

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4: gb-on.\*

5: gb-ov.\*

6: gb-ph.\*

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11: gb-ro.\*

12: gb-sv.\*

13: gb-vi.\*

14: gb-vi.\*

15: en-ba.\*

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[illegible]











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Matches 70; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 3 AGCATCGATCTCTAACACGCTACCGCTTACCGTACGCTGACCGCGGTGTCCT 62
DB 118 AGAGTCCTTACGACGCTCTCTCATATCTTTGTTGTTCCCGATTGTTCTAT 59

QY 63 ACAGCGCTTAAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 58 CTGAGCGTAAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

RESULT 8
AF519993/c
LOCUS
DEFINITION
Populus tremula x Populus tremuloides transgenic line
Bach5:358-Ac-rolC3 with Zea mays Ac element, partial
AF519993
ACCESSION
VERSION
KEYWORDS
ORGANISM
Populus tremula x Populus tremuloides
Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosid 1; Malpighiales; Salicaceae; Salicaceae; Populus.
Kumar S. and Fladung M.
AUTHORS
TITLE
Somatic mobility of the maize element Ac and its usability for gene
tagging in aspen (2002) In press
JOURNAL
Plant Mol. Biol. 2002
REFERENCE
Kumar S. and Fladung M.
Direct Submission
Submitted (06-JUN-2002) Bundesforschungsanstalt fuer Forst- und
Landwirtschaft, Institut fuer Forstgenetik und
Forstzucht, Forstwissenschaft, Steier Landesforste 2, Grosshansdorf 22927,
Germany
FEATURES
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Matches 39; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 42 GGTAGACCGGGGTGTGTGCTACAGGATGAACCGGTGCTACGCTGCTGTAATACT 101
DB 124 GGAAACAGAGGTCCTCTTACTTACGATGAACCGGTGCTACGCTGCTGAATACC 65

QY 102 ACGCGATTTCCTACTCTCTTCA 127

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Db
64 TCTACGTTTCCTTCATTTTAA 39

RESULT 9
AF433042/c
LOCUS
DEFINITION
Cloning vector pWS31, complete sequence.
AF433042
ACCESSION
VERSION
KEYWORDS
ORGANISM
Cloning vector pWS31
Cloning vector pWS31
artificial sequences; vectors.
Suzuki J, Ogasawara P, Volpe T, Howard S, Jones J, D.,
Dean C, Ma H, and Martensen R.
Patterns of gene action in plant development revealed by enhancer
trap and gene trap transposable elements
Genes Dev. 9 (14), 1797-1810 (1995)
95147957
PUBMED
7622040
REFERENCE
2 (bases 1 to 8975)
de la Bastide M., Preston R., O'Shaughnessy A., May B.,
Martensen R., and McCombie W.R.
Direct Submission
Submitted (15-OCT-2001) Cold Spring Harbor Laboratory, 1 Bungtown
Rd, Cold Spring Harbor, NY 11724, USA
FEATURES
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1..8975
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organism="Cloning vector pWS31"
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transformation of Arabidopsis thaliana"
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	Best Local Similarity	81.0%; Pred. No. 0.03; Indels 0; Gaps 0;
	Matches	47; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
ay	62	GTTACGAAAGCGGTGGTCTGACGAGATGAACAACGTCGGTAGCAGTGCGTGAATAA 99
bb	58	GTTACGAAAGCGGTGGTCTGACGAGATGAACAACGTCGGTAGCAGTGCGTGAATAA 1
RESULT 15		
LOCUS	AF519991/c	716 bp DNA linear SYN 14-JUL-2002
DEFINITION	Populus tremula x Populus tremuloides transgenic line	
DESCRIPTION	EchS3;35S-Ac-roIC43 isolate SK41 with Zea mays Ac element, partial sequence.	
VERSIONS	AF519991.1 GI:21745065	
ORGANISM	Populus tremula x Populus tremuloides	
REFERENCE	Populus tremula x Populus tremuloides Bokaryte, Viridiplantae; Rosales, Eubryophyta, Tracheophyta; Rosaceae, Maloideae; Salicaceae; Saliceae; Populus; Eurosidia; Malpighiales; Salicaceae; Populus; 1 (bases 1 to 716)	
AUTHORS	Kumar,S. and Pfandung,M.	
TITLE	Somatic mobility of the maize element Ac and its usability for gene transfer into Populus	
JOURNAL	Plant Mol. Biol. (2002) In press	
REFERENCE	2 (bases 1 to 716)	
AUTHORS	Kumar,S. and Pfandung,M.	
JOURNAL	Submitted (06-JUN-2002) Bundesforschungsanstalt fuer Forst- und Holzwirtschaft, Institut fuer Forschungsetnik und Forstpflanzenzüchtung, Sieker Landstrasse 2, Grosshansdorf 22927, Germany Location/Qualifiers	
FEATURES	1..716	
source	/organism='Populus tremula x Populus tremuloides' /mol_type='genomic DNA' /db_xref='taxon:541' /isolate='SK41' /db_xref='taxon:47664' /sex='female' /rsm_type='leaf' /note='transgenic line EchS3;35S-Ac-roIC43'	
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ORIGIN		
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Best Local Similarity	71.6%; Pred. No. 0.031;	
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Qy	65	AGCGATGAACCGTCGTAAGTCGGTAAATACTACGGGATTTTCCCATCTACT 124
Dd	92	AGCGATGAACCGTCGTAAGTCGGTAAATACTACGGGATTTTCCCATCTACT 124
Qy	125	TCTCTCCGGCGWAC 138
Dd	32	TTAAC TTCGGGAC 19
Search completed:	May 16, 2004, 13:58:08	
Job time:	2974 secs	

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iclaic - nucleic search, using sw model  
n: May 16, 2004, 10:18:15, Search time 397 Seconds  
2899,303 Million cell updates/sec

US-09-071-033-2  
icet score: 271  
nct: 1 GAGCATGATCTTAAACA.....CTACTCATGAGCTCTTCTT 271

ng table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

hed: 3373863 sears, 2124059041 residues

. number of hits satisfying chosen parameters: 6747726

num DB seq length: 2000000000

Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- ase :
- 1: Geneseq2 25Jan04:\*
  - 2: Geneseq1 980a:\*
  - 3: Geneseq1 2001a:\*
  - 4: Geneseq2 2001a:\*
  - 5: Geneseq2 2001b:\*
  - 6: Geneseq2 2002a:\*
  - 7: Geneseq2 2002b:\*
  - 8: Geneseq2 2003a:\*
  - 9: Geneseq2 2003b:\*
  - 10: Geneseq2 2004a:\*

Read No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

lt	Query	Score	Match	Length	DB	ID	Description
1	271	100.0	3	100.0	3	AAR4066	Arabidops
2	127.4	47.0	3	100.0	3	AAR4065	Arabidops
3	127.4	47.0	4071	3	AAA34063	AAA34063	Arabidops
4	39.4	14.5	4810	7	ABX23541	ABX23541	NM encod
5	39.4	14.5	4565	7	ABX93541	ABX93541	NM encod
6	32.9	11.4	4565	7	ABX93542	ABX93542	Transpos
7	32.4	12.0	495	5	AA578905	AA578905	DNA encod
8	31.6	11.6	3632	4	AB119247	AB119247	Drosophi
9	31.6	11.7	2971	4	AB128815	AB128815	Drosophi
10	31.6	11.7	3037	4	AB120065	AB120065	Drosophi
11	31.6	11.7	3037	4	AB120065	AB120065	Drosophi
12	31.6	11.7	3308	4	AB128824	AB128824	Drosophi
13	31.6	11.7	10400	4	AB120064	AB120064	Drosophi
14	31.6	11.7	10418	4	AB128814	AB128814	Drosophi
15	31.6	11.7	10451	4	AB119246	AB119246	Drosophi
16	30.8	11.4	1395	6	ABX78986	ABX78986	Chicken a
17	30.8	11.4	2065	6	ABQ75903	ABQ75903	Chicken a
18	30.8	11.4	5769	4	AAR43560	AAR43560	Human: imm
19	30.8	11.4	6162	4	AAR43551	AAR43551	Human: imm
20	30.8	11.4	6168	4	AAR43557	AAR43557	Human: imm
21	30.8	11.4	6232	4	AAR43552	AAR43552	Human: imm
22	30.8	11.4	6232	4	AAR43552	AAR43552	Human: imm
23	30.8	11.4	6261	4	AAR43554	AAR43554	Human: imm
24	30.2	11.1	1022	4	AAR43471	AAR43471	Human: col

c	24	30.2	11.1	1381	6	ABQ61034	Abq61034 bkt bins
c	25	30.2	11.0	519	5	AAR41226	Pyrococcus
c	26	29.6	10.9	978	6	ABQ31473	Abq31473 Oligonuc
c	28	29.6	10.9	978	6	ABQ31472	Abq31472 Oligonuc
c	29	29.6	10.9	1565	6	AAQ70588	AAQ70588 Influenza
c	30	29.6	10.9	1986	5	AAR42043	DNA encod
c	32	29.4	10.8	1565	3	AAC37656	Arabidops
c	33	29.4	10.8	1775	4	AAR45194	Chrysaerth
c	34	29.4	10.8	1943	7	AAQ72605	AAQ72605 Rice gene
c	35	29.4	10.8	2990	4	AB114452	Drosophil
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c	38	29.4	10.8	6746	6	ABX35498	Human end
c	39	29.4	10.8	6746	6	ABX35498	Human end
c	41	29.2	10.8	4748	2	AAQ24508	Gene 519
c	42	29.2	10.7	2000	7	AAQ24508	Gene 519
c	43	28.9	10.7	19639	2	AAQ33524	Rice gene
c	44	28.9	10.6	5199	4	AAQ33524	Rice gene
c	45	28.9	10.6	5199	4	AAQ33524	Rice gene

## ALIGNMENTS

RESULT 1	AAA94066	standard; DNA; 271 BP.
ID	AAA94066	
AC	AAA94066;	
DT	30-JUN-2001	(first entry)
XX	Arabidopsis thaliana sporycoteless spl Ds element sequence.	
XX	Arabidopsis thaliana sporycoteless spl Ds element sequence.	
XX	Arabidopsis thaliana sporycoteless spl Ds element sequence.	
KW	Sporycoteless; spl; meiocyte formation; plant sterility; seedless fruit;	
KW	pollenless flower; Ds element; ds.	
XX	Arabidopsis thaliana.	
XX	Arabidopsis thaliana.	
XX	Arabidopsis thaliana.	
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FT	misc_feature	/notes="4 base pair duplication due to Ds element insertion"
FT	misc_feature	64..133
FT	misc_feature	/tag="a" element"
FT	misc_feature	134..137
FT	misc_feature	/tag="b" element"
FT	misc_feature	/notes="4 base pair duplication due to Ds element insertion"
DN	WO200056907-A1.	
PD	28-SEP-2000.	
PR	22-MAR-1999;	99MO-SG000023.
PR	22-MAR-1999;	99MO-SG000023.
XX	(WOLE) INST MOLECULAR AGROBIOLOGY.	
XX	Ye D, Yang W, Sundaresan V, Xu G;	
XX	WPT; 2000-59457/56.	

not a human

parent

Sporycoteless nucleic acids and polypeptides, useful for controlling sporycote or meiocyte formation in plants for producing transgenics that bear seedless fruits and/or pollenless flowers.

PS Claim 4; Fig 1A; 65pp; English.

CC The present sequence comprises part of the coding sequence for the Arabidopsis thaliana sporocytless (spl) protein containing the Ds element. The present sequence is involved in the formation of microspores in male plants and megasporocytes in female plants. The mutant gene was isolated from a collection of transposants due to its male and female sterile phenotype. The mutation is caused by the insertion of the Ds element between bases 411 and 412 of the gene. The insertion of the Ds element causes the formation of the sterile phenotype in plants caused by the insertion of the Ds element. CC can be used to produce transgenic plants which contain the Ds element or antisense sequences to the gene, enabling the production of seedless fruits, pollenless flowers and plants with a larger biomass

XX Sequence 271 BP; 57 A; 71 C; 69 G; 74 T; 0 U; 0 Other;

Query Match 100.0%; Score 271; DB 3; Length 271; Best Local Similarity 100.0%; Pred. No. 4e-88; Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTAGCATGCTCTACACAGCTACCGCTTTTACCGTACGGTGAACCCGGGTGTG 60

DB 1 GTAGCATGCTCTACACAGCTACCGCTTTTACCGTACGGTGAACCCGGGTGTG 60

QY 61 CTACAGGATGAACCGGTGCTGAAGCGGTGAATTAATCTACGGATTTTCCATCT 120

DB 61 CTACAGGATGAACCGGTGCTGAAGCGGTGAATTAATCTACGGATTTTCCATCT 120

QY 121 ACTTTCATTCGCGGTGCTGAGCTTCCCAAGCTCATCGGAGACAGCATCTATGTG 180

DB 121 ACTTTCATTCGCGGTGCTGAGCTTCCCAAGCTCATCGGAGACAGCATCTATGTG 180

QY 181 TGGAGTCGGTTCGGTCAAGCTTATGATACACCGGTATTTCTGATGGGTTTGTGA 240

DB 181 TGGAGTCGGTTCGGTCAAGCTTATGATACACCGGTATTTCTGATGGGTTTGTGA 240

QY 241 GAGCTCTCACTACTATGAGCTCTCTCA 271

DB 241 GAGCTCTCACTACTATGAGCTCTCTCA 271

RESULT 2

ID AAA94065 standard; cDNA; 1302 BP.

XX AAA94065;

XX AAA94067;

DT 30-JAN-2001 (first entry)

DE Arabidopsis thaliana sporocytless spl coding sequence.

XX Sporocytless; spl; meiocyte formation; plant sterility; seedless fruit; pollenless flower; Ds element; ss.

XX Arabidopsis thaliana.

EH Key Location/Qualifiers

FT 80..1024

FT /\*tag= a

FT /product= "SPL"

FT /trans\_except= [pos.146..149,aa.149]

XX W0200056907-A1.

XX 28-SEP-2000.

XX 22-MAR-1999; 99NO-SG000023.

XX 22-MAR-1999; 99NO-SG000023.

XX (MOLE-) INST MOLECULAR AGROBIOLOGY.

XX

PS Claim 4; Fig 1A; 65pp; English.

CC The present sequence comprises part of the coding sequence for the Arabidopsis thaliana sporocytless (spl) protein. This protein is involved in the formation of microspores in male plants and megasporocytes in female plants. The mutant gene was isolated from a collection of transposants due to its male and female sterile phenotype. The mutation is caused by the insertion of the Ds element between bases 411 and 412 of the gene. The insertion of the Ds element causes the formation of the sterile phenotype in plants caused by the insertion of the Ds element. CC can be used to produce transgenic plants which contain the Ds element or antisense sequences to the gene, enabling the production of seedless fruits, pollenless flowers and plants with a larger biomass

XX Sequence 1302 BP; 402 A; 273 C; 275 G; 352 T; 0 U; 0 Other;

Query Match 47.0%; Score 127.4; DB 3; Length 1302; Best Local Similarity 96.6%; Pred. No. 1.4e-35; Matches 139; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 132 GCGCTCAAGGCTTCGAGCTCA-TGGGCGACACGATCTATGTCGATCGG 190

DB 410 GTCTCAAGGCTTCGAGCTCACTCGGAGACAGCATCTATGTCGATCGG 469

QY 191 TGGGTCAGCTATGATGACACCGGTATTTCTGATGGGTTTCTGACCTCTCC 250

DB 470 TGGGTCAGCTATGATGACACCGGTATTTCTGATGGGTTTCTGACCTCTCC 529

QY 251 ACTACTCATGAGCTCTCTCA 271

DB 530 ACTCTGAGAGCTCTCTCA 550

RESULT 2

ID AAA94067 standard; DNA; 4071 BP.

XX AAA94067;

DT 30-JAN-2001 (first entry)

DE Arabidopsis thaliana sporocytless spl promoter and coding sequence.

XX Sporocytless; spl; meiocyte formation; plant sterility; seedless fruit; pollenless flower; Ds element; ds.

XX Arabidopsis thaliana.

EH Key Location/Qualifiers

FT Promoter

FT 7..5650

FT /\*tag= a

FT CDS

FT 2691..3822

FT /\*tag= b

FT /product= "SPL"

XX W0200056907-A1.

XX 28-SEP-2000.

XX 22-MAR-1999; 99NO-SG000023.

XX 22-MAR-1999; 99NO-SG000023.

XX (MOLE-) INST MOLECULAR AGROBIOLOGY.

XX



26-DEC-2002

TO  
LATE

KW Activator element; Ac; transposable element; Da element; transposon;  
 KW gamete-specific promoter; suicide gene; gametophytic suicide trait; GSR;  
 KW se.  
 CC  
 CC  
 CC Zea mays.  
 CC  
 CC WO200164926-A2.  
 CC  
 CC  
 CC 07-SEP-2001.  
 CC  
 CC 28-FEB-2000; 2001WO-US006249.  
 CC  
 CC 28-FEB-2000; 2000US-0185524P.  
 CC  
 CC (UYTA ) UNIV YALE.  
 CC  
 CC Dellaporta SL, Moreno MA;  
 CC WPT; 2001-602569/68.  
 CC Genetic construct for the control of transgenes in transgenic plants  
 CC comprises a sex-specific promoter operatively linked to a suicide gene  
 CC that selects against male or female gametes containing the suicide gene.  
 CC  
 CC Example 1; Page 73-74; 81pp; English.

CC The present sequence represents a maize Activator element (Ac), which is  
 CC a transposable element. 5' and 3' fragments of the present sequence were  
 CC used to synthesize a synthetic Da element, which was used to  
 CC produce the construct of the invention. The Da element comprises a  
 CC nucleic acid construct, comprising a male gamete- or female gamete-  
 CC specific promoter operatively linked to a suicide gene, both of which are  
 CC linked to a gene of interest, a transposable element, a transposon and  
 CC heterologous traits in plants. It also provides the unwanted spread of  
 CC the element in the plant. The element also provides the unwanted spread of  
 CC the selection of a gametophytic suicide trait (GSR) and for  
 CC the selection of unlinked transpositions. The construct is applicable for  
 CC any commercially grown plant, including fruit, seed, oil, protein or hay  
 CC and for any other plant or animal. The construct is suitable for control,  
 CC landclearing, green manure, producing food additive, pulp and seed  
 CC production and smoking products

CC Sequence 4565 BP; 1344 A; 994 C; 978 G; 1249 T; 0 U; 0 Other;

Query Match 14.4%; Score 39; DB 4; Length 4565;  
 Best Local Similarity 76.2%; Pred. No. 0.0045;  
 Matches 48; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 65 AGGATGAAAACGGTCGGTACGTCGGTAAATACCTACCGATTTTCCATCTACTT 124

DB 2 AGGATGAAAACGGTCGGTACGTCGGTAAATACCTACCGATTTTCCATCTACTT 61

QY 125 TCA 127

DB 62 TAA 64

RESULT 6

ID ABR93542/C

ABR93542 standard; DNA; 4565 BP.

ABR93542;

06-JUN-2003 (first entry)

Transposable element associated nucleic acid.

de; transposition modification; gene repression; antibiotic resistance;  
 human gamete; transplant; shoot; heart disease; phenylketonuria;  
 Alzheimer's disease; aging; emphysema; cancer; osteoporosis; diabetes;  
 Kluver-Bucchi syndrome; multiple sclerosis; multiple sclerosis; diabetes;  
 muscular atrophy; breast cancer; stroke; multiple sclerosis; blindness;  
 cataract; attention deficit disorder; dyslexia; hypertension;

KW schizophrenia; depression; bulimia nervosa; migraine; anorexia nervosa;  
 KW Alzheimer's disease; metabolic disorder; blood clotting;  
 KW hemophilia; diabetes; schizophrenia; attention deficit disorder;  
 KW pregnancy associated disease; infertility; obesity; gastroenteritis;  
 KW immune system disorder; blood cell surface antigen recognition disease;  
 KW nondisjunction; epilepsy; spinal cord disorder; pituitary gland disease;  
 KW autoimmune disease; osteoarthritis; cystic fibrosis; arterial disease;  
 KW mania; cardiomyopathy.

XX Unidentified.

OS US2002199216-A1.

PW 26-DEC-2002.

PD 01-MAY-2002; 2002US-00139221.

PP 01-MAY-2001; 2001US-0287882P.

PR (MNCN)/ MACRAE A F.

XX Macrae AF;

PI Macrae AF;

DR WPI; 2003-329935/31.

XX Modifying transcription within an organism or repressing transcription of  
 CC targeted gene within a cell, by introducing transposase encoding effector  
 CC molecule into organism or introducing transposase element into cell.

XX Disclosure; Page 34-37; 46pp; English.

CC The invention relates to a method of modifying (increasing, decreasing or  
 CC altering) transcription within an organism or repressing transcription of  
 CC at least one targeted gene within a cell comprising introducing a  
 CC transposase element into the organism or introducing a  
 CC transposase element into the cell, thereby increasing transcription of the  
 CC (increasing, decreasing or altering) transcription within an organism or  
 CC for repressing transcription of at least one targeted gene within a cell.  
 CC The method is useful for determining the functions of unknown function  
 CC transcription within an organism and transcription of a gene encoding  
 CC antibiotic resistance, for repressing targeted genes within human gametes  
 CC (sperm and eggs). The method is useful for repressing transcription within  
 CC a micro-organism system. The method is useful for repressing transcription for  
 CC repressing transcription within a transplanted organ, shoot or body  
 CC part. The method is also useful for modifying the expression of genes  
 CC associated with heart disease, phenylketonuria, Alzheimer's disease,  
 CC multiple sclerosis, muscular dystrophy, emphysema, sickle cell anemia,  
 CC disease, glaucoma, blindness, cataracts, attention deficit disorder,  
 CC dyslexia, hypertension, schizophrenia, mania, depression, bulimia  
 CC nervosa, anorexia nervosa, stroke, heart attack, allergies,  
 CC Kluver-Bucchi syndrome, attention deficit disorder, osteoporosis, erectile  
 CC dysfunction, infertility, immune system disorders, blood cell surface  
 CC antigen recognition disease, nondisjunction, epilepsy, obesity,  
 CC psoriasis, spinal cord disorders, pituitary gland disorders,  
 CC attention deficit disorder, attention deficit disorder, attention deficit disease  
 CC and cardiomyopathy. The present sequence represents the transposable  
 CC element associated nucleic acid. Note: the present sequence is shown in  
 CC the appendix of the specification but no reference is made to it  
 CC elsewhere in the specification

Sequence 4565 BP; 1249 A; 978 C; 994 G; 1344 T; 0 U; 0 Other;

Query Match 14.4%; Score 39; DB 7; Length 4565;

Best Local Similarity 76.2%; Pred. No. 0.0045;  
 Matches 48; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 65 AGGATGAAAACGGTCGGTACGTCGGTAAATACCTACCGATTTTCCATCTACTT 124

DB 4564 ABR93542/C  
 4564 ABR93542 standard; DNA; 4565 BP; 1249 A; 978 C; 994 G; 1344 T; 0 U; 0 Other;







XX (PERK) PE CORP NY.  
 XX Venter JC, Adams M, Li PWD, Myers EW;  
 XX WPI; 2001-656860/75.  
 XX  
 XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 XX genes from Drosophila and for elucidating cell signaling and cell-cell  
 XX interactions.  
 XX  
 XX Claim 1; SEQ ID NO 37015; 21pp + Sequence Listing; English.  
 XX  
 XX The invention relates to an isolated nucleic acid detection reagent  
 XX capable of detecting 1000 or more genes from Drosophila. The invention is  
 XX useful in developmental biology and in elucidating cell signaling and  
 XX cell-cell interactions in higher eukaryotes for the development of  
 XX insecticides, therapeutics and pharmaceutical drugs. The invention  
 XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 XX clones genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
 XX ABB72072). The sequence data for this patent did not form part of the  
 XX printed specification, but was obtained in electronic format directly  
 XX from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
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 XX Sequence 10418 BP; 2884 A; 2143 C; 2343 G; 3038 T; 0 U; 0 Other;  
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 XX Best Local Similarity 52.2%; Pred. No. 3.3;  
 XX Matches 70; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
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 XX 1253 ATACACGACATCATCTGCGAGCTCCAGCCGACAGCCAGCAGCCACCCACATGTC 1194  
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 XX 187 CGGCTGGGCTGAGTATGATGACCCGGTATTTTCATCGGGTTTGTGAGACCTC 246  
 XX 1193 CGCCCGGAGTGGCTATGACGACAGGCGCATTTGATGCTCTCTGAGCGTGC 1134  
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 XX 247 CTCCTACTCTG 260  
 XX 1133 GTCCCATCTCATG 1120  
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 XX  
 XX ABL19246;  
 XX  
 XX 26-MAR-2002 (first entry)  
 XX  
 XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 9211.  
 XX  
 XX Drosophila; developmental biology; cell signalling; insecticide;  
 XX Pharmaceutical; gens; ds.  
 XX  
 XX Drosophila melanogaster.  
 XX  
 XX W0200171042-A2.  
 XX  
 XX 27-SEP-2001.  
 XX  
 XX 23-MAR-2001; 2001WO-US009231.  
 XX  
 XX 23-MAR-2000; 2000US-0191637P.  
 XX  
 XX 11-JUN-2000; 2000US-00614150.  
 XX  
 XX (PERK) PE CORP NY.  
 XX  
 XX Venter JC, Adams M, Li PWD, Myers EW;  
 XX WPI; 2001-656860/75.  
 XX  
 XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 XX genes from Drosophila and for elucidating cell signaling and cell-cell  
 XX interactions.  
 XX  
 XX Claim 1; SEQ ID NO 9211; 21pp + Sequence Listing; English.  
 XX  
 XX The invention relates to an isolated nucleic acid detection reagent  
 XX capable of detecting 1000 or more genes from Drosophila. The invention is  
 XX useful in developmental biology and in elucidating cell signaling and  
 XX cell-cell interactions in higher eukaryotes for the development of  
 XX insecticides, therapeutics and pharmaceutical drugs. The invention  
 XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 XX clones genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
 XX ABB72072). The sequence data for this patent did not form part of the  
 XX printed specification, but was obtained in electronic format directly  
 XX from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 10451 BP; 2904 A; 2145 C; 2346 G; 3056 T; 0 U; 0 Other;  
 XX  
 XX Query Match 11.7%; Score 31.6; DB 4; Length 10451;  
 XX Best Local Similarity 52.2%; Pred. No. 3.3;  
 XX Matches 70; Conservative 0; Mismatches 64; Indels 0; Gaps 0;  
 XX  
 XX 127 ATCCGGCTGACAGAGCTTCCCAAGCTCATCGAGCAGACAGATATATGTGTGAGT 186  
 XX 1253 ATACACGACATCATCTGCGAGCTCCAGCCGACAGCCAGCAGCCACCCACATGTC 1194  
 XX  
 XX 187 CGGCTGGGCTGAGTATGATGACCCGGTATTTTCATCGGGTTTGTGAGACCTC 246  
 XX 1193 CGCCCGGAGTGGCTATGACGACAGGCGCATTTGATGCTCTCTGAGCGTGC 1134  
 XX  
 XX 247 CTCCTACTCTG 260  
 XX 1133 GTCCCATCTCATG 1120  
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 XX RESULT 15  
 XX ABL079896/c  
 XX ID ABL079896 standard; cDNA; 1395 BP.  
 XX  
 XX ABL079896;  
 XX  
 XX 23-DEC-2002 (first entry)  
 XX  
 XX Chicken acetylglucosamine transferase VI (Gnt VI) protein encoding cDNA.  
 XX  
 XX Acetylglucosamine transferase VI; Gnt VI; GLNac; N-glucan; chicken;  
 XX gene; ss.  
 XX  
 XX Gallus gallus.  
 XX  
 XX Key Location/Qualifiers  
 XX CDS 1..1395  
 XX /cseg= "Gnt VI"  
 XX /note= "acetylglucosamine transferase VI protein"  
 XX  
 XX JF20020209597-A.  
 XX  
 XX 30-JUL-2002.  
 XX  
 XX 18-JAN-2001; 2001JP-00010883.  
 XX  
 XX 18-JAN-2001; 2001JP-00010883.  
 XX  
 XX (PURE ) FUJIREBIO KK.  
 XX  
 XX WPI; 2002-670039/72.  
 XX  
 XX F-PS08; ABB82145.  
 XX  
 XX An acetylglucosamine transferase VI protein.  
 XX  
 XX Claim 5; Page 11-13; 22pp; Japanese.

The invention relates to a protein having acetylglucosamine transferase VI (Gnt VI) activity and polynucleotides encoding the Gnt VI protein. The protein can be expressed by standard recombinant technology. Gnt VI is a member of the alpha-mannosidase family of glycosyl hydrolases. It is located in the core structure of N-glycan. The present sequence represents the chicken Gnt VI protein coding sequence

Sequence 1395 BP; 280 A; 444 C; 366 G; 305 T; 0 U; 0 Other;  
 100% Match 11.4%; Score 30.8; DB 6; Length 1395;  
 100% Local Similarity 48.8%; Pred. No. 2.6;  
 100% Cons. 83; Conservative 0; Mismatches 87; Indels 0; Gaps 0;  
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 1143 CTGCACCCCGACCGCGGTGTGTGTCTACAGGATGAACCGTCTGGTAAGCTCGTA 1084  
 95 AATCTACGCGATTTTTCCTATCTTCTACGCGGTGTGTGTCTACAGGATGAACCGTCTGGTAAGCTCGTA 154  
 1083 AACTCTGTGGTTTTTTCCTATCTTCTACGCGGTGTGTGTCTACAGGATGAACCGTCTGGTAAGCTCGTA 1024  
 135 ATCGGAGATACAGGATTTTTCCTATCTTCTACGCGGTGTGTGTCTACAGGATGAACCGTCTGGTAAGCTCGTA 204  
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GenCore version 5.1.6  
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US-09-701-023-2

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# SUMMARIES

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1	29	10.7	592	2	US-08-475-891A-3	Sequence 3, Appl
2	27.4	10.1	777	4	US-09-252-991A-12771	Sequence 12771, A
3	27.4	10.1	2577	4	US-09-252-991A-13185	Sequence 13185, A
5	27.4	10.1	5332	4	US-09-601-861-3	Sequence 3, Appl
6	27.4	10.1	161652	4	US-09-497-855A-40	Sequence 40, Appl
7	27.2	10.0	948	4	US-09-252-991A-12820	Sequence 12820, A
8	27.2	10.0	1074	4	US-09-134-001C-2128	Sequence 18033, A
9	27	10.0	1074	4	US-09-539-331D-127	Sequence 2128, Ap
10	27	10.0	1001	4	US-09-539-331D-127	Sequence 127, Appl
11	27	10.0	111282	4	US-08-754-250-3	Sequence 3, Appl
12	26.8	9.9	822	3	US-08-524-525-383	Sequence 383, Appl
14	26.8	9.9	903	3	US-08-609-593A-37	Sequence 37, Appl
14	26.8	9.9	903	3	US-08-937-399-37	Sequence 37, Appl
15	26.8	9.9	903	3	US-09-310-367-37	Sequence 37, Appl
16	26.8	9.9	903	3	US-08-464-231-37	Sequence 37, Appl
17	26.8	9.9	903	3	US-08-929-525-23	Sequence 23, Appl
19	26.8	9.9	2236	3	US-08-609-593A-23	Sequence 23, Appl
20	26.8	9.9	2236	3	US-08-937-399-23	Sequence 23, Appl
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22	26.8	9.9	2236	3	US-08-464-231-23	Sequence 23, Appl
24	26.8	9.9	2236	3	US-09-454-231-23	Sequence 23, Appl
25	26.6	9.8	587	4	US-09-833-381-1690	Sequence 1690, Ap
26	26.6	9.8	1317	4	US-09-016-434-1446	Sequence 1446, Ap
27	26.6	9.8	1576	4	US-09-358-138-134	Sequence 134, App

## ALIGNMENTS

```

RESUME 1
US-08-475-891A-3/C
; Sequence 3, Application US/08475891A
; Patent No. 5859319
; GENERAL INFORMATION
; INVENTOR: Pamela C.
; APPLICANT: Wang, Guo-Liang
; APPLICANT: Song, Wen-Yang
; TITLE OF INVENTION: Procedures and Materials for Confering
; TITLE OF INVENTION: Disease Resistance in Plants
; TITLE OF INVENTION: Disease Resistance in Plants
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US 08/475,891A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,375
; APPLICATION NUMBER: 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; TELEPHONE: (415) 576-0300
; TELECOMMUNICATION INFORMATION:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRAND: single
; TOPOLOGY: linear
; FEATURE TYPE: DNA (genomic)
; NAME/KEY: CDS
; LOCATION: join(512..3149, 3993..4393)
; OTHER INFORMATION: /product=tax;key=chromas upp. disease
; OTHER INFORMATION: resistance gene RRR-B from rice (Oryza

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Sequence 281, App  
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Sequence 115, Appl  
Sequence 8976, Ap  
Sequence 15, Appl  
Sequence 3, Appl  
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Sequence 15, Appl  
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Sequence 7, Appl  
Sequence 9, Appl  
Sequence 12, Appl  
Sequence 22, Appl

28 26.6 9.8 2731 4 US-09-976-594-281  
29 26.6 9.8 3823 4 US-09-512-250C-1  
30 26.6 9.8 15894 1 US-08-348-891A-1  
31 26.6 9.8 15894 1 US-08-905-817-1  
32 26.4 9.7 1595 4 US-08-905-817-1  
33 26.4 9.7 1335 3 US-09-621-976-8976  
34 26.2 9.7 1335 3 US-08-954-536-15  
35 26.2 9.7 1378 5 PCT-US91-08479-3  
36 26.2 9.7 2866 4 US-09-784-864-30  
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ADDRESS: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036/2711  
COMPUTER READABLE FORM:  
NAME: Pennie & Edmonds  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT VERSION: 2.0  
APPLICATION NUMBER: US/08/829,525  
FILING DATE: 28-MAR-1997  
CLASSIFICATION: 536  
PRIORITY DOCUMENT:  
APPLICATION NUMBER: US 08/609,583  
FILING DATE: 01-MAR-1996  
APPLICATION NUMBER: US 08/487,748  
FILING DATE: 01-JUN-1996  
APPLICATION NUMBER: US 08/398,633  
FILING DATE: 03-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Cotruzzini, Laura A.  
FIRM: Cotruzzini, Laura A.  
TELEPHONE: 212-790-5090  
TELEFAX: 212-790-5090  
TELEX: 66141 PNNIE  
FIRM ADDRESS:  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
JUNTER, H. R. B. Chair  
TYPE: nucleic acids

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RESULT 14
US-09-609-983A-37/C
; Sequence 37, Application US/08609583A
; Patent No. 6204171
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; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF TWINKLE DISORDERS

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CITY: New York  
STATE: New York  
COUNTRY: USA  
CONTAINER NUMBER: 609-588A-11  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
SOFTWARE: PASEFO Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/609,588A  
CLASSIFICATION: 1-1996  
CLASSIFICATION CODE: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/487,748  
CLASSIFICATION: 1-1996  
APPLICATION NUMBER: US 08/398,633  
FILING DATE: 03-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: STEVEN J. LAURIA  
ADDRESS: 100 LAURA AVE.  
NEW YORK, NY 10017-4742  
REFERENCE/DOCKET NUMBER: 7853-048  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
FAX: 212-790-9090  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1000 bp  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE: 121 UNK

Query Match 9.9%; Score 26.8; DB 3; Length 903;

Best Local Similarity 46.7%; Pred. No. 4.8;  
Matches 85; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY	84	AACGGTCGGTAAATACTACGGGATTTTCCCATCTCTACTCTTCATCCCGGCTACAGGC	143
DB	380	AACTTCAGATTAATTTTTCATCATTTATATCCCTGGATTTGGATCCCGAGCAGTAG	321
QY	144	TTCCCAAGCTCATCGGAGACACAGAGCATATATGTGTGGAGTGGGTCCGGTCAGGTTA	203
DB	320	ATCCCACTCTCTGTAGAGTCAACATCTCTATATGGTAGGAGACACATCTCTCTGGAAA	261
QY	204	TGATCGACCGGTTATTTCTTCCATGGGGTTTGGTGAAGCTCTCCACTACTCATGAGC	263
DB	260	TCCCATTTAGCCAGTATCTGGATGTCATTAATTCATCTCTTTCATGCTCTGAGC	201
QY	264	TC 265	
DB	200	AC 199	

Search completed: May 16, 2004, 14:53:11  
Job time : 79 secs

# RESULT 15

US-08-937-399-37/c

; Sequence 37; Application US/08937399

; Patent No. 6288218

; GENERAL INFORMATION:

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

; TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESS: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; PRIORITY: 60/400,711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE VERSION: Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/937,399

; FILING DATE:

; PRIORITY DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/609,583

; FILING DATE: 01-MAR-1996

; APPLICATION NUMBER: US/08/487,748

; FILING DATE: 01-MAR-1995

; APPLICATION NUMBER: US/08/398,633

; FILING DATE: 03-MAR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 742

; REFERENCE/DOCKET NUMBER: 7853-048

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-790-9090

; TELEFAX: 212-790-9084

; TELEMAIL: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 37:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 903 base pairs

; STRAND: single

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; US-08-937-399-37

## Query Match

Best Local Similarity 46.7%; Pred. No. 4.8;

Matches 85; Conservative 0; Mismatches 97; Indels 0; Gaps 0;



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; GENERAL INFORMATION:
; APPLICANT: Dellaporta, Stephen L.
; APPLICANT: Dellaporta, Maria A.
; APPLICANT: Yalcin, Yavuz A.
; TITLE OF INVENTION: Methods and Compositions to Reduce or Eliminate
; FILE REFERENCE: 44574-5078-US /09/794,384A
; CURRENT FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/185,524
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 1: Patentin Ver. 2.1
; SEQ ID NO 3: Patentin Ver. 2.1
; LENGTH: 4565
; TYPE: DNA
; FEATURE:
; FEATURE: Zeta maye
; OTHER INFORMATION: Transposable element Ac
; US-09-794-384A-3

Query Match 14.44; Score 39; DB 9; Length 4565;
Best Local Similarity 76.34; Pred No 0.0025;
Matches 48; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 65 AGCGTAAAGAGCGGTGGTAAAGCGTGAATAAATACAGCGAATTTTCCATCTACTT 124
DB 125 TCA 127
DB 62 TAA 64

RESULT 3 221-8/C
; Sequence 8: Application US/10138221
; Publication No. US20020159216A1
; GENERAL INFORMATION:
; APPLICANT: Amy P. MacRae OF TRANSDUCIBLE ELEMENTS FOR ALTERING GENE EXPRESSION
; FILE REFERENCE: 51178/7
; CURRENT FILING DATE: 2002-08-01
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/287,882
; NUMBER OF SEQ ID NOS: 9 05-01
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; SEQ ID NO 9
; LENGTH: 4565
; TYPE: DNA
; ORGANISM: Zeta maye
; US-10-138-221-8

Query Match 14.44; Score 39; DB 14; Length 4565;
Best Local Similarity 76.34; Pred No 0.0025;
Matches 48; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 65 AGCGTAAAGAGCGGTGGTAAAGCGTGAATAAATACAGCGAATTTTCCATCTACTT 124
DB 125 TCA 127
DB 4504 TAA 4502

RESULT 4
; Sequence 213703, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

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; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.1159
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 213703
; SEQ ID NO 213704
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-213703

Query Match 12.34; Score 33.4; DB 13; Length 533;
Best Local Similarity 52.44; Pred No 0.12;
Matches 70; Conservative 1; Mismatches 62; Indels 0; Gaps 0;

QY 125 TCATCGCGGCTTAAGAGGTTCCCAAGCTCTCGCGAGCAGCGATCTATGTGTGTGA 184
DB 336 TCATCTGACCTGATGTTTCCCTCATCTCATCTGAGAGACGCTGGTTTGGTATGTA 277
DB 185 CTCGCGTCGGTGTGGTTTGTATGATGACCGGTTATTTTCATGCGGTTTGTGAGCC 244
DB 276 AGCGAGAGAGAGAGAGATGTGCTCCGATGTAAATGCGGAGTCAATTTCTGTACT 217
QY 245 TCCTCACTACTC 257
DB 216 CCTGCGCCATTC 204

RESULT 5
; Sequence 632-213704/C
; Publication No. US20020198371A1
; Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.1159
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-30
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 213704
; SEQ ID NO 213705
; LENGTH: 533

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TYPE: DNA
ORGANISM: Human
>027-632-213704

Query Match 12.3%; Score 33.4; DB 13; Length 533;
Local Similarity 52.6%; Pred. No. 0.12;
Ches 70; Conservative 1; Mismatches 62; Indels 0; Gaps 0;

125 TATCCCGGCTACAGAGCTTCCCAAGCTCTCCGAGGACACAGAGATCTATGTGTGGA 184
336 TATCTCTGCTGAGTGGTGGCTCTGATCATCGAGGAGCGGGTTCCTGTATGTA 277
185 GTGCGTCCGGTCAGGTATGATGACCCGGTATTTCTCCATCGGGTTTTGTGAGCC 244
276 ACGAAGAGGAGGAGTATGTATGGTCCCAAGGTGAATGCGGGGTGATTTCTTGACT 217
245 TCTCTCCACTACT 257
216 CCTTCCCAATTC 204

>027-632-213703/c
Sequence 213704, Application US/10027632
Publication No. US20030204075A9
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
PRIORITY FILING DATE: 2002-04-20
PRIORITY FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-26
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: US 60/144,000
SOFTWARE: FRANSISQ for Windows Version 4.0
SEQ ID NO 213704
LENGTH: 533
TYPE: DNA
ORGANISM: Human
US-10-027-632-213704

Query Match 12.3%; Score 33.4; DB 16; Length 533;
Local Similarity 52.6%; Pred. No. 0.12;
Ches 70; Conservative 1; Mismatches 62; Indels 0; Gaps 0;

QY 125 TATCCCGGCTACAGAGCTTCCCAAGCTCTCCGAGGACACAGAGATCTATGTGTGGA 184
DB 336 TATCTCTGCTGAGTGGTGGCTCTGATCATCGAGGAGCGGGTTCCTGTATGTA 277
QY 185 GTGCGTCCGGTCAGGTATGATGACCCGGTATTTCTCCATCGGGTTTTGTGAGCC 244
DB 276 ACGAAGAGGAGGAGTATGTATGGTCCCAAGGTGAATGCGGGGTGATTTCTTGACT 217
QY 245 TCTCTCCACTACT 257
DB 216 CCTTCCCAATTC 204

RESULT 8
US-10-425-114-3402/c
Sequence 3402, Application US/10425.114
Publication No. US200405488A1
GENERAL INFORMATION
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Chen, Xian
APPLICANT: Tabaka, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425.114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 71128
SEQ ID NO 3402
SEQ ID NO 3403
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 70264066_EJ2
US-10-425-114-3402

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TYPE: DNA
ORGANISM: Human
>027-632-213704

Query Match 12.3%; Score 33.4; DB 13; Length 533;
Local Similarity 52.6%; Pred. No. 0.12;
Ches 70; Conservative 1; Mismatches 62; Indels 0; Gaps 0;

125 TATCCCGGCTACAGAGCTTCCCAAGCTCTCCGAGGACACAGAGATCTATGTGTGGA 184
336 TATCTCTGCTGAGTGGTGGCTCTGATCATCGAGGAGCGGGTTCCTGTATGTA 277
185 GTGCGTCCGGTCAGGTATGATGACCCGGTATTTCTCCATCGGGTTTTGTGAGCC 244
276 ACGAAGAGGAGGAGTATGTATGGTCCCAAGGTGAATGCGGGGTGATTTCTTGACT 217
245 TCTCTCCACTACT 257
216 CCTTCCCAATTC 204

>027-632-213703/c
Sequence 213703, Application US/10027632
Publication No. US20030204075A9
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
PRIORITY FILING DATE: 2002-04-20
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-26
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FRANSISQ for Windows Version 4.0
SEQ ID NO 213703
LENGTH: 533
TYPE: DNA
ORGANISM: Human
US-10-027-632-213703

Query Match 12.3%; Score 33.4; DB 16; Length 533;
Local Similarity 52.6%; Pred. No. 0.12;
Ches 70; Conservative 1; Mismatches 62; Indels 0; Gaps 0;

125 TATCCCGGCTACAGAGCTTCCCAAGCTCTCCGAGGACACAGAGATCTATGTGTGGA 184
336 TATCTCTGCTGAGTGGTGGCTCTGATCATCGAGGAGCGGGTTCCTGTATGTA 277
185 GTGCGTCCGGTCAGGTATGATGACCCGGTATTTCTCCATCGGGTTTTGTGAGCC 244
276 ACGAAGAGGAGGAGTATGTATGGTCCCAAGGTGAATGCGGGGTGATTTCTTGACT 217
245 TCTCTCCACTACT 257
216 CCTTCCCAATTC 204

>027-632-213704/c
Sequence 213704, Application US/10027632
Publication No. US20030204075A9
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027.632
PRIORITY FILING DATE: 2002-04-20
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-26
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FRANSISQ for Windows Version 4.0
SEQ ID NO 213704
LENGTH: 533
TYPE: DNA
ORGANISM: Human
US-10-027-632-213704

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351 TACGCTACTTGGGGGCTCCCGCTTACCTGTATATCGGACACAGTGGCTCCCTTGT 292
153 TATTCGGAGG 163
291 GATCTCGGC 281

T 12
-006-285-506/c
lication 506, Application US/10006285
lication No. US200301698541
BRAL INFORMATION: Cunningham
PLICANT: Matthew R. Kaser
TLE OF INVENTION: MARKER GENES RESPONDING TO TREATMENT WITH TOXINS
LE REFERENCE: PA-0319 US
SERIES NUCLEOTIDE NUMBER: US/10/006-285
PARENT FILING DATE: 2003-12-05
MBER OF SEQ ID NOS: 514
FTWARE: PERL Program
ID NO 506
ID NO 159
TYPE DNA
RGANISM: Homo sapiens
EATURE:
AME/KEY: misc feature
AME/KEY: Feature
AME/KEY: Incomplete
LOCATION: 1183-1314, 1485-1577
THER INFORMATION: a, t, c, g, or other
-006-285-506

xy Match 11.1%; Score 30.2; DB 15; Length 1759;
t Local Similarity 51.9%; Pred. No. 3.1;
ches 68; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

33 ACCCTCAGCTGACGCGGGTGTGCTACAGGATGAAAGCGTGGTAAGCTCGG 92
815 ACACGAATATGTTGACCGGGGTCGAGGAGGTGCAAGAAAGCGCTTCCACATCGA 756
93 TAAATATACGGATTTTTCGACTACTTTCACCGGGGTACAGGCTTCCAGCTTCGAGC 152
755 TACGCTACTGGGCGCTCCGCTTCACTGTATATCGGACACAGTGGCTCCCTTGT 696

153 TATTCGGAGG 163
695 GATCTCGGC 685

T 13
-006-192-451
rence 451, Application US/10087192
lication No. US200201025861
BRAL INFORMATION: David W.
PLICANT: Morris, David W.
PLICANT: Morris, David W.
TLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TLE REFERENCE: 5294500012 US/10/087,192
SERIES NUCLEOTIDE NUMBER: US/10/087,192
PARENT FILING DATE: 2002-03-01
FOR APPLICATION NUMBER: US 09/747,377
FOR FILING DATE: 2000-12-22
FOR APPLICATION NUMBER: US 09/798,566
FOR FILING DATE: 2000-09-02
MBER OF SEQ ID NOS: 2053
FTWARE: FastSeq for Windows Version 4.0
ID NO 451
ID NO 159
LENGTH: 256525
TYPE DNA
RGANISM: Mus musculus
EATURE:

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NAME/KEY: misc feature
LOCATION: (1)...(256525)
OTHER INFORMATION: n = A,T,C or G
US-10-087-192-451

Query Match 10.9%; Score 29.6; DB 13; Length 256525;
Best Local Similarity 59.3%; Pred. No. 38;
Matches 50; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

OY 106 GATTTTCCTCATCTACTTTCATCCCGGGCTACAGGCTTCCCAAGCTTCATCGGAGCA 165
DB 106805 GCTTTTCCCATCATCTCCCTCCCATCTCCCATGTGTTCAAAATAGTCTCGGCTT 106864
OY 166 CAGGCTCATCTGCGGATCGG 189
DB 106865 TAGGCGCTAGCATGTGTGAAGATGG 106886

RESULT 14
US-09-919-497-18
Sequence 18, Application US/09919497
Patent No. US20030106662A1
NAME/KEY: misc feature
AME/KEY: Feature
AME/KEY: Incomplete
APPLICANT: Muter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
SERIES NUCLEOTIDE NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
FOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SERIES NUCLEOTIDE NUMBER: US/09/919,497
FTWARE: Patentin version 3.0
ID NO 18
ID NO 18
LENGTH: 6746
TYPE: DNA
ORGANISM: Homo sapiens
US-09-919-497-18

Query Match 10.8%; Score 29.4; DB 9; Length 6746;
Best Local Similarity 55.3%; Pred. No. 10;
Matches 57; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

OY 98 TACTACGGGATTTTCCCATCTACTTTCATCCCGGGCTACAGGCTTCCCAAGCTATC 157
DB 1928 TACTAAGGGGTTTCTCTTCATCGGCATCTCCCAAGCTCTCGGCTGCTGCTGCTTC 1987
OY 158 GZAGCAACAGGATCTATCTGTGTGAGTCCGCTCGGCTGAGG 200
DB 1988 AGCAACCCCATCTTACTTGTGTGGAGTGCGGTGTGGCATG 2030

RESULT 15
US-09-967-768A-303
Sequence 303, Application US/09967768A
Patent No. US20030150877A1
NAME/KEY: misc feature
AME/KEY: Feature
AME/KEY: Incomplete
APPLICANT: Augustus, Menna
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
FILE REFERENCE: 68929006
SERIES NUCLEOTIDE NUMBER: US/05/967,768A
CURRENT FILING DATE: 2001-09-28
FOR APPLICATION NUMBER: US/60/236,109
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,034
PRIOR FILING DATE: 2000-09-28
FOR APPLICATION NUMBER: US/60/236,111
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 325
SERIES NUCLEOTIDE NUMBER: US/05/967,768A
FTWARE: Patentin version 3.0
ID NO 303
ID NO 303
LENGTH: 6746
TYPE: DNA

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! ORGANISM: Homo sapiens  
US-09-967-768A-303

Query Match 10.88; Score 29.4; DB 9; Length 6746;  
Best Local Similarity 55.38; Pct Id 10;  
Matches 57; Conservative 0; Mismatches 46; Indels 0; Gaps 0;  
QY 98 TACTACGGGATTTTCCCATCTCTACTTTTATCTCGGGATACAGGCTTCCCAAGCTGATC 157  
DB 1928 TACTAAGGGTTTCTCTCTCATCGGCAATCTCCAGGATCTCGAGCTGTGCGCTTC 1987  
QY 158 GGGAGCAACAGGATCTATGTGTGGAGTCGGTGGGTCTGG 200  
DB 1968 AGCAACCCCATCTCTGTGTGGAGTGGGTGTGGGATG 2030

Search completed: May 16, 2004, 15:00:17  
Job time : 416 secs





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GENE 1 (bases 1 to 282)
THOR Kim.C.M., Piao.H.L., Park.S.J., Chon.N.S., Je.B.I., Sun.B.,
Park.S.H., Park.Y.J., Lee.E.J., Kim.M.J., Lee.J.J., Nam.M.H.,
Rapid, large-scale generation of B8 transposant lines and analysis
of De loci in rice
JMAL Unpublished (2003)
INT Divisat Chong, Hwan
Gyeongang National University
Gaeje-dong 900, Jinju 660-701, South Korea
Tel: +82 55 751 6029
Fax: +82 55 751 6025
Email: cchanon@ga.gnu.ac.kr
THOR Location: chromosome 10 clone OSUNBa0035r15
JMAL Class: transposon-tagged.
JMAL Location/Qualifiers
JMAL   /organism="Oryza sativa (japonica cultivar-group)"
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ity Match Local Similarity 14.4% Score 39; DB 29; Length 282;
Chas 48; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
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125 TCA 127
209 TAA 211
J 5 CF31337 393 bp mRNA linear EST 18-AUG-2003
TION NACL-07-G19 bl Rice callus plasmid cDNA library (NACL) Oryza
sation CF31338
ION CF31338.1 GI:33810894
TUS Oryza sativa
JANISM Oryza sativa
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Oryza;
1 (bases 1 to 392)
Kim.J.S., Jun.K.M., Cheong.P.J., Kim.M.J., Lee.T.H., Shin.Y.C.,
Song.S.I., Kim.J.K., Kim.Y.-K. and Nahm.B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
JENCE Genomics and Genetics Institute, Greengene Biotech Inc.; Division
THOR of BioScience and Bioinformatics, Myongui University
JMAL 1 (bases 1 to 392)
JMAL Location/Qualifiers
JMAL   /organism="Oryza sativa"
JMAL   /mol_type="mRNA"
JMAL   /cultivar="Nackdong"
JMAL   /db_xref="xref:Nackdong"
JMAL   /clone_lib="NACL-07-G19"
JMAL   /issue_type="callus"
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JMAL   /lab_host="S.coli DH108"
JMAL   /note="vector: pCR-TOPO; Site 1: EcoRI; mRNA was capped
JMAL   with oligoribonucleotides and then used as templates for
JMAL RT-PCR."
JES Query Match 14.4% Score 39; DB 14; Length 393;
source Best Local Similarity 14.4% Score 39;
Matches 48; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 65 AGGATGAAACCGGTGGTAAATCGGTAAATCTACGGAATTTTCCCATCTACTT 124
DB 2 AAGGATGAAACCGGTGGTAAATCGGTAAATCTACGGAATTTTCCCATCTACTT 61
QY 125 TCA 127
DB 62 TAA 64

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